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PATENT APPLICATION
Attorney Docket No. 15966-539 CIP (Cura-39 CIP)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT: Rothberg et al.
SERIAL NO.: 09/614,505
FILING DATE: July 11, 2000
FOR: METHOD FOR IDENTIFYING A BIOMOLECULE

EXAMINER: Janell T. Cleveland
ART UNIT: 1655

Box AF
Commissioner for Patents
Washington, D.C. 20231

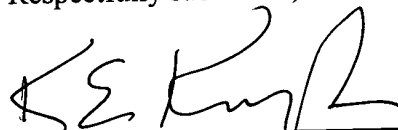
TRANSMITTAL LETTER

Transmitted herewith for filing in the present application are the following documents:

1. Response to Office Action dated April 11, 2002 (10 pages);
2. Petition for a Two Month Extension of Time (1 page);
3. Check for \$200.00 (# 13998) pursuant to 37 C.F.R. §1.17(a)(2); and
4. Return Postcard

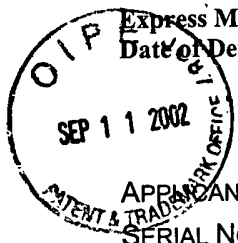
It is believed that no additional fees are due. However, if any fees are to be adjusted, the Commissioner is hereby authorized to charge any balance due, or credit any overpayment, to the undersigned's account, Deposit Account No. 50-0311, Reference No. 15966-539 CIP (Cura 39CIP). A duplicate copy of this transmittal letter is enclosed.

Respectfully submitted,



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Date: September 11, 2002



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Date of Deposit: September 11, 2002

Attorney Docket No. 15962-539

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPlicant(S): Rothberg et al.
SERIAL NO.: 09/614,505
FILING DATE: July 11, 2000
FOR: Method for Identifying a Biomolecule

EXAMINER: Janell T. Cleveland
ART UNIT: 1655

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Response to Office Action Dated April 11, 2002

In response to the Office Action dated April 11, 2002 ("Office Action"), please amend the application as follows.

In the Claims:

Cancel claims 27-57 without prejudice.

Add the new claims as follows:

58. A method of identifying a nucleic acid sequence, the method comprising:

- (a) providing one or more populations of nucleic acid molecules comprising at least one set of nucleic acid sequences;
- (b) digesting the one or more populations of nucleic acid molecules with one or more restriction enzymes to produce one or more subpopulations of nucleic acid molecules;
- (c) partitioning said subpopulations to produce one or more partitioned fractions;
- (d) constructing a library from each said partitioned fraction, wherein said library comprises specific nucleic acid fragments arrayed to generate mapping information of its original location in the partitioned fraction;
- (e) pooling said specific fragments from said library, wherein the pooling further provides for mapping a fragment's original location;
- (f) partitioning said pooled fragments to provide one or more selected subsets;
- (g) identifying a specific fragment from one or more selected subsets;
- (h) mapping the specific fragment to its original location; and
- (i) sequencing said specific fragment, thereby identifying a nucleic acid sequence.